



Sequence Listing

<110> ASHKENAZI, AVI J
BOTSTEIN, DAVID
DODGE, KELLY H.
GURNEY, AUSTIN L.
KIM, KYUNG JIN
LAWRENCE, DAVID A.
PITTI, ROBERT
ROY, MARGARET A
TUMAS, DANIEL B
WOOD, WILLIAM I.

<120> DcR3 Polypeptide, A TNFR Homolog

<130> P1134R2 REVISED

<140> US 09/157,289

<141> 1998-09-18

<150> US 60/059,288

<151> 1997-09-18

<150> US 60/094,640

<151> 1998-07-30

<160> 18

<210> 1

<211> 300

<212> PRT

<213> Homo sapiens

<400> 1

Met Arg Ala Leu Glu Gly Pro Gly Leu Ser Leu Leu Cys Leu Val
1 5 10 15

Leu Ala Leu Pro Ala Leu Leu Pro Val Pro Ala Val Arg Gly Val
20 25 30

Ala Glu Thr Pro Thr Tyr Pro Trp Arg Asp Ala Glu Thr Gly Glu
35 40 45

Arg Leu Val Cys Ala Gln Cys Pro Pro Gly Thr Phe Val Gln Arg
50 55 60

Pro Cys Arg Arg Asp Ser Pro Thr Thr Cys Gly Pro Cys Pro Pro
65 70 75

Arg His Tyr Thr Gln Phe Trp Asn Tyr Leu Glu Arg Cys Arg Tyr
80 85 90

Cys Asn Val Leu Cys Gly Glu Arg Glu Glu Glu Ala Arg Ala Cys	95	100	105
His Ala Thr His Asn Arg Ala Cys Arg Cys Arg Thr Gly Phe Phe	110	115	120
Ala His Ala Gly Phe Cys Leu Glu His Ala Ser Cys Pro Pro Gly	125	130	135
Ala Gly Val Ile Ala Pro Gly Thr Pro Ser Gln Asn Thr Gln Cys	140	145	150
Gln Pro Cys Pro Pro Gly Thr Phe Ser Ala Ser Ser Ser Ser Ser	155	160	165
Glu Gln Cys Gln Pro His Arg Asn Cys Thr Ala Leu Gly Leu Ala	170	175	180
Leu Asn Val Pro Gly Ser Ser Ser His Asp Thr Leu Cys Thr Ser	185	190	195
Cys Thr Gly Phe Pro Leu Ser Thr Arg Val Pro Gly Ala Glu Glu	200	205	210
Cys Glu Arg Ala Val Ile Asp Phe Val Ala Phe Gln Asp Ile Ser	215	220	225
Ile Lys Arg Leu Gln Arg Leu Leu Gln Ala Leu Glu Ala Pro Glu	230	235	240
Gly Trp Gly Pro Thr Pro Arg Ala Gly Arg Ala Ala Leu Gln Leu	245	250	255
Lys Leu Arg Arg Arg Leu Thr Glu Leu Leu Gly Ala Gln Asp Gly	260	265	270
Ala Leu Leu Val Arg Leu Leu Gln Ala Leu Arg Val Ala Arg Met	275	280	285
Pro Gly Leu Glu Arg Ser Val Arg Glu Arg Phe Leu Pro Val His	290	295	300

<210> 2
 <211> 1114
 <212> DNA
 <213> Homo sapiens

<220>
 <221> Unsure
 <222> 1090

<223> Unknown base

<400> 2

tccgcaggcg gaccgggggc aaaggaggtg gcatgtcggc caggcacagc 50
agggtcctgt gtccgcgctg agccgcgctc tccctgctcc agcaaggacc 100
atgagggcgc tggaggggccc aggcctgtcg ctgctgtgcc tgggtgttggc 150
gctgcctgcc ctgctgccgg tgccggctgt acgcggagtg gcagaaacac 200
ccacctaccc ctggcgggac gcagagacag gggagcggct ggtgtgcgcc 250
cagtgcctccc caggcacctt tgtgcagcgg ccgtgccgcc gagacagccc 300
cacgacgtgt ggcccgtgtc caccgcgcca ctacacgcag ttctggaact 350
acctggagcg ctgccgctac tgcaacgtcc tctgcgggga gcgtgaggag 400
gaggcacggg cttgccacgc caccacaac cgtgcctgcc gctgccgcac 450
cggcttcttc gcgcacgctg gttctgtctt ggagcacgca tcgtgtccac 500
ctggtgccgg cgtgattgcc ccgggcaccc ccagccagaa cacgcagtgc 550
cagccgtgcc cccagggcac cttctcagcc agcagctcca gctcagagca 600
gtgccagccc caccgcaact gcacggccct gggcctggcc ctcaatgtgc 650
caggctcttc ctcccatgac accctgtgca ccagctgcac tggcttcccc 700
ctcagcacca gggaccagg agctgaggag tgtgagcgtg ccgtcatcga 750
ctttgtggct ttccaggaca tctccatcaa gaggtgcag cggctgctgc 800
aggccctcga ggccccggag ggctggggtc cgacaccaag ggcgggccgc 850
gcggccttgc agctgaagct gcgtcggcgg ctcacggagc tectgggggc 900
gcaggacggg gcgctgctgg tgccggctgt gcaggcgtg cgcgtggcca 950
ggatgcccgg gctggagcgg agcgtccgtg agcgttctct ccctgtgcac 1000
tgatcctggc cccctcttat ttattctaca tccttggcac ccacttgca 1050
ctgaaagagg ctttttttta aatagaagaa atgaggtttn ttaaaaaaaaa 1100
aaaaaaaaaa aaaa 1114

<210> 3

<211> 491

<212> DNA
<213> Unknown

<220>

<223> Unknown organism

<220>

<221> unsure

<222> 62, 73, 86, 98

<223> unknown base

<400> 3

gccgagacag cccacgacg tgtggcccg gtccaccgc ccactacag 50
cagttctgga antaactgga gcncctgccg tactgnaacg tcctctgngg 100
ggagcgtgag gaggaggcac gggcttgcca cgccaccac aaccgtgct 150
gccgctgccg caccggcttc ttgcgcacg ctggtttctg cttggagcac 200
gcacgtgtc cacctggtgc cggcgtgatt gccccgggca ccccgagcca 250
gaacacgcag tgcttagccg tgccccccag gcaccttctc agccagcagc 300
tccagctcag agcagtgccg gcccaccgc aactgcacgg ccctgggcct 350
ggccctcaat gtgccaggct cttcctccca tgacaccctg tgcaccagct 400
gcactggctt cccctcagc accagggtac caggagctga ggagtgtgag 450
cgtgccgtca tcgactttgt ggctttccag gacatctcca t 491

<210> 4

<211> 73

<212> DNA

<213> Unknown

<220>

<223> Unknown organism

<400> 4

gccgagacag cccacgacg tgtggcccg gtccaccgc ccactacag 50
cattctggaa ctacctggag cgc 73

<210> 5

<211> 271

<212> DNA

<213> Unknown

<220>

<223> Unknown organism

<220>

<221> unsure

<222> 42, 62, 73, 86, 98, 106, 120, 122, 153, 167, 184, 220, 233

<223> unknown base

<400> 5

gccgagacag ccccacgacg tgtggcccg gtccaccgcn actacacg 50

cagttctgga antaactgga gcncctgccgc tactgnaacg tcctctgngg 100

ggagcntgag gaggaggcan gngcttgcca cgccaccac aaccgcgcct 150

gngctgcag caccggnctt ctcgcgcacg ctgntttctg cttggagcac 200

gcacgtgtc cacctggtgn cggcgtgatt gcncgggca cccccagcca 250

gaacacgcat gcaaagccgt g 271

<210> 6

<211> 201

<212> DNA

<213> Unknown

<220>

<223> Unknown organism

<220>

<221> unsure

<222> 182

<223> unknown base

<400> 6

gcagttctgg aactacctgg agcgtgccg ctactgcaac gtcctctgcg 50

gggagcgtga ggaggaggca cgggcttgcc acgccacca caaccgtgcc 100

tgccgctgcc gcaccggctt cttcgcgcac gctggtttct gcttgagca 150

cgcacgtgt ccacctggtg ccggcgtgat tccccgggc accccagcc 200

a 201

<210> 7

<211> 277

<212> DNA

<213> Unknown

<220>

<223> Unknown organism

<220>

<221> unsure

<222> 142

<223> unknown base

<400> 7

gaggggcccc caggagtggg ggccggaggt gtggcagggg tcaggttgct 50
ggccccagcc ttgcaccctg agctaggaca ccagttcccc tgaccctgtt 100
cttccctect ggctgcaggc acccccagcc agaacacgca gnccagccgt 150
gccccccagg cacctttctca gccagcagct ccagctcaga gcagtgccag 200
ccccaccgca actgcacggc cctgggcctg gccctcaatg tgccaggctc 250
ttcttcccat gacaccctgt gcaccag 277

<210> 8

<211> 199

<212> DNA

<213> Unknown

<220>

<223> Unknown organism

<400> 8

gcatcgtgtc cacctgggtg cggcgtgatt gccccgggca cccccagcca 50
gaacacgcag gcctagccgt gccccccagg cacctttctca gccagcagct 100
ccagctcaga gcagtgccag cccccaccgca actgcacggc cctgggcctg 150
gccctcaatg tgccaggctc ttcttcccat gacaccctgt gcaccagct 199

<210> 9

<211> 226

<212> DNA

<213> Unknown

<220>

<223> Unknown organism

<220>

<221> unsure

<222> 4, 9, 12, 165

<223> unknown base

<400> 9

agcngtgcnc cncaggcacc ttctcagcca gcagttccag ctçagagcag 50

tgccagcccc accgcaactg cacggccctg ggccctggccc tcaatgtgcc 100
 aggcctcttcc tcccatgaca cgctgtgcac cagctgcact ggcttcccc 150
 tcagcaccag ggtancagga gctgaggagt gtgagcgtgc cgctcatcgac 200
 tttgtggctt tccaggacat ctccat 226

<210> 10
 <211> 283
 <212> DNA
 <213> Homo sapiens

<220>
 <221> Unsure
 <222> 1-283
 <223> Unknown organism

<220>
 <221> unsure
 <222> 27, 64, 140
 <223> unknown base

<400> 10
 cttgtccacc tgggtgccggc gtgattnccc gggcaccccc agccagaaca 50
 cgcagtgccca gccntcccc caggcacctt ctcagccagc agctccagct 100
 cagagcagtg ccagccccac cgcaactgca acgccctggn ctggccctca 150
 atgtgccagg ctcttctctc catgacaccc tgtgcaccag ctgcactggc 200
 ttccccctca gcaccagggt accaggagct gaggagtgtg agcgtgccgt 250
 catcgacttt gtggctttcc aggacatctc cat 283

<210> 11
 <211> 21
 <212> DNA
 <213> Unknown

<220>
 <223> Unknown organism

<400> 11
 cacgctgggt tctgcttgga g 21

<210> 12
 <211> 22
 <212> DNA

<213> Unknown

<220>

<223> Unknown organism

<400> 12

agctggtgca caggggtgtca tg 22

<210> 13

<211> 53

<212> DNA

<213> Unknown

<220>

<223> Unknown organism

<400> 13

cccaggcacc ttctcagcca gccagcagct ccagctcaga gcagtgccag 50

ccc 53

<210> 14

<211> 24

<212> DNA

<213> Unknown

<220>

<223> Unknown organism

<400> 14

acacgatgcg tgctccaagc agaa 24

<210> 15

<211> 17

<212> DNA

<213> Unknown

<220>

<223> Unknown organism

<400> 15

cttcttcgcg cacgctg 17

<210> 16

<211> 16

<212> DNA

<213> Unknown

<220>

<223> Unknown organism

<400> 16
atcacgccgg caccag 16

<210> 17
<211> 461
<212> PRT
<213> Homo sapiens

<400> 17
Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu
1 5 10 15
Leu Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr
20 25 30
Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr
35 40 45
Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly
50 55 60
Gln His Ala Lys Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys
65 70 75
Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val
80 85 90
Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser Asp Gln Val
95 100 105
Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys Thr Cys
110 115 120
Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys Arg
125 130 135
Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala
140 145 150
Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala
155 160 165
Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg
170 175 180
Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser
185 190 195
Arg Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala
200 205 210

Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln	215	220	225
His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser	230	235	240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr	245	250	255
Gly Asp Phe Ala Leu Pro Val Gly Leu Ile Val Gly Val Thr Ala	260	265	270
Leu Gly Leu Leu Ile Ile Gly Val Val Asn Cys Val Ile Met Thr	275	280	285
Gln Val Lys Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val	290	295	300
Pro His Leu Pro Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu	305	310	315
Gln Gln His Leu Leu Ile Thr Ala Pro Ser Ser Ser Ser Ser Ser	320	325	330
Leu Glu Ser Ser Ala Ser Ala Leu Asp Arg Arg Ala Pro Thr Arg	335	340	345
Asn Gln Pro Gln Ala Pro Gly Val Glu Ala Ser Gly Ala Gly Glu	350	355	360
Ala Arg Ala Ser Thr Gly Ser Ser Asp Ser Ser Pro Gly Gly His	365	370	375
Gly Thr Gln Val Asn Val Thr Cys Ile Val Asn Val Cys Ser Ser	380	385	390
Ser Asp His Ser Ser Gln Cys Ser Ser Gln Ala Ser Ser Thr Met	395	400	405
Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro Lys Asp Glu Gln	410	415	420
Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser Gln Leu Glu	425	430	435
Thr Pro Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro Leu Pro	440	445	450
Leu Gly Val Pro Asp Ala Gly Met Lys Pro Ser	455	460	

<210> 18

<211> 293

<212> PRT

<213> Homo sapiens

<400> 18

Met Asn Lys Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser
1 5 10 15

Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His
20 25 30

Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro
35 40 45

Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr
50 55 60

Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His
65 70 75

Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu
80 85 90

Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys
95 100 105

Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys
110 115 120

His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr
125 130 135

Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe
140 145 150

Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn
155 160 165

Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr
170 175 180

His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys
185 190 195

Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala
200 205 210

Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val Asp
215 220 225

Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile
230 235 240

Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys
245 250 255

Leu Trp Lys His Gln Asn Lys Ala Gln Asp Ile Val Lys Lys Ile
260 265 270

Ile Gln Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile
275 280 285

Gly His Ala Asn Leu Thr Phe Glu
290